

```

MM of: US-09-294-298-2 to: GenEmbl: * out_format : pfs
Date: Jan 19, 2001 12:18 AM
about: Results were produced by the GenCore software, version 4.5,
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command line parameters:
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-Q/-cgn2.1/-USPTO.spool/US03294298/runat_17012001_125501_27756/app_query.fasta_1
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-FGAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
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search information block:
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  query length: 1423
  database: GenBank;*
  database sequences: 1118133
  database length: -173092196
  search time (sec): 10440.680000

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0.000000	+	7057.50
0.000000	+	6894.00
0.000000	+	6885.50
0.000000	+	6308.50
0.000000	+	4064.00
0.000000	-	4059.50
0.000000	+	3987.00
0.000000	+	3620.50
0.000000	+	1257.50
0.000000	+	1257.50
0.000000	-	1257.50
0.000000	+	1257.50
0.000000	+	1201.00
0.000000	+	1092.50
0.000000	+	1088.50
0.000000	+	1080.50
0.000000	+	906.00
0.000000	-	710.00
0.000000	+	676.50
0.000000	+	650.50
0.000000	+	613.00
0.000000	+	600.00
0.000000	+	531.00
0.000000	+	502.00
0.000000	+	488.50
0.000000	+	479.50
0.000000	-	479.00
0.000000	+	455.00
0.000000	+	437.50
0.000000	+	437.50
0.000000	+	433.50
0.000000	+	431.00
0.000000	+	430.50
0.000000	+	429.50
0.000000	+	420.00
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: pfs

are, version 4.5,
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  query: US-09-294-298-2
  query length: 1423
  database: GenBank;*
  database sequences: 1118133
  database length: -173092196
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0.000000	+	7451.00
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0.000000	+	6308.50
0.000000	+	4064.00
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0.000000	+	1201.00
0.000000	+	1092.50
0.000000	+	1088.50
0.000000	+	1080.50
0.000000	+	906.00
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0.000000	+	676.50
0.000000	+	650.50
0.000000	+	613.00
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0.000000	+	531.00
0.000000	+	502.00
0.000000	+	488.50
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0.000000	-	479.00
0.000000	+	455.00
0.000000	+	437.50
0.000000	+	437.50
0.000000	+	433.50
0.000000	+	431.00
0.000000	+	430.50
0.000000	+	429.50
0.000000	+	420.00
0.000000	-	417.00
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0.000000	+	394.50
0.000000	+	381.00

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9b	-rc-mm1	AE055993	+	360.50	180.82	0.0648	21.1	1

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1			
1			
1			
34 ysIleIleSerGlyAspGlnLeuLeuMetLeuAspGluAspGluIle			
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151 CCCCTCTGATCGAACCGAGGGAGTCAGCCGAAACAAACAA			
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84 IutYtYHisLeuGlyIleArgSerArgGlySerValProGlyGlylys			
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1987

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LOCUS AF058790
DEFINITION ratmus norvegicus

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 AF050183.2 GI:10140854
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 Rattus.
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 AUTHORS Kim, J.H., Liao, D., Lau, L.F. and Huganir, R.L.
 TITLE SynGAP: a synaptic RasGAP that associates with the PSD-95/SAP90 protein family

MEDLINE 9B240917
 2 (bases 1 to 4265)
 REFERENCES Kim, J.H. and Huganir, R.L.
 AUTHORS Direct Submission
 TITLE Submitted (20-FEB-1998) Neuroscience, Johns Hopkins Medical
 JOURNAL Institute, 725 N. Wolfe Street, PCRM 900, Baltimore, MD 21205, USA
 SOURCE On Sep 15, 2000 this sequence version replaced gi:3044054.
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 variants: SngdAP-a and SngdAP-b"

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VERSION	AF048976..1	GI:2935447	
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;;			
Rattus;			
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AUTHORS	Chen, H.-J. and Kennedy, M.B.		
TITLE	Identification and cloning of a novel 130 kd protein containing a ras GTPase-activating domain from the rat forebrain postsynapti...		
JOURNAL	TIME SOC. NEUROSCI.: ASTR.: 1466;(1997)		
REFERENCE	2. (bases 1 to 4063)		
AUTHORS	Chen, H.-J., ROTAS, T.M. and KENNEDY, M.B.		
TITLE	A synaptic Ras GTPase-activating protein (p135 SyngAP) inhibited by		
JOURNAL	CAM kinase II.		
UNPUBLISHED			
REFERENCE	3. (bases 1 to 4063)		
AUTHORS	Chen, H.-J. and Kennedy, M.B.		
TITLE	Direct Submission		
JOURNAL	Submitted 17 FEB 1998; Division of Biology, California Institute		
OF TECHNOLOGY, 1200 E. California Blvd., MC 216-16, Pasadena, CA	91125, USA		
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 AUTHORS Suzuki,T.
 TITLE SYNGAP-d
 JOURNAL Published Only in DataBase (1999) In press
 REFERENCE 2 (bases 1 to 4801)
 AUTHORS Suzuki,T.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-1998) to the DDBJ/EMBL/GenBank databases. Tatsuo Suzuki, Shinshu University School of Medicine, Department of Neuroplasticity; 3-1-1 Asahi, Matsuoto, Nagano 390-8621, Japan (E-mail:suzukit@sch.md.shinshu-u.ac.jp, Tel:+81-263-37-2683, Fax:+81-263-37-225)
 COMMENT On Mar 16, 1999 this sequence replaced g1:4239945.
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----- Summary Statistics -----
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Sequencing vector: plasmid; L08752; 100% of reads
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Chemistry: Dye-primer Big dye; 0% of reads
Consensus quality: 145680 bases at least Q40
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Insert size: 148326, 10.8% error; agarose-fp
Quality coverage: 6.43x in Q20 bases; sum-of-contigs Quality
coverage: 6.54x in Q20 bases; agarose fp

* NOTE: this is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

*      1. 54611: contig of 54611 bp in length
*          * 54612 54711: gap of 100 bp
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out_format : pfs

Date: Jan 19, 2001 7:43 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (C) 1993-2000 Compigne Ltd.

Command line parameters:
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-DEL0P=100.000 -TRANS=human4.0.con -LIST=45 -DOCALIGN=200 -THR_SCORE=pot
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Date: Jan 19, 2001 2:41 AM
About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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Database: N_Geneseq_36.*  

Database sequences: 480022
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/SIDSB6/gcdata/geneseq/NA2000.DAT:T87318 + 255.50 162.26 0.2997 36778 1 CC The sequence given is a lengthened version of the Type I GTPase activating protein (GAP) GAP6. It has additional DNA 5' to GAP6 and
/SIDSB6/gcdata/geneseq/NA1998.DAT:T092263 + 253.50 172.30 0.0827 7918 1 CC encodes a protein with a molecular weight of 116,000 daltons. This is similar to the molecular weight of the GAP protein purified from human
/SIDSB6/gcdata/geneseq/NA1999.DAT:T06978 + 252.00 177.05 0.0450 3632 1 CC placenta. GAP is thought to be a cytoplasmic protein which stimulates
/SIDSB6/gcdata/geneseq/NA1999.DAT:T1373 + 252.00 177.05 0.0450 3632 1 CC normal ras p21 GTPase activity but does not effect the GTPase activity
/SIDSB6/gcdata/geneseq/NA1999.DAT:T81748 + 251.50 162.30 0.2982 26338 1 CC associated with oncogenic mutants. This sequence or fragments derived
/SIDSB6/gcdata/geneseq/NA1995.DAT:T80016 + 251.00 185.85 0.0145 4456 1 CC from it can be useful as cancer diagnostics, being partic. useful to
/SIDSB6/gcdata/geneseq/NA1992.DAT:T060202 + 251.00 169.65 0.1162 8937 1 CC diagnose for ras p21 related cancers.
/SIDSB6/gcdata/geneseq/NA1997.DAT:T6941 + 251.00 168.30 0.1381 10706 1 XX Sequence 4307 BP; 1280 A; 857 C; 956 G; 1214 T; 0 other;
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 DT 22-MAY-1991 (first entry)

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Date: Jan 18, 2001 9:24 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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-Q=cgn2_2.1/USPTO_spool/US03294398/runat.17012001.125501_27745/app_query.fasta_1.4359
-DE=EST_QFMT fastap -SUFFIX=_EST -GAPOP=12,000 -GAPEXT=4,000
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-QGAPEXT=0,050 -XGAPOP=0,000 -XGAPEXT=0,500 -FGAOP=6,000
-FGAPEXT=7,000 -YGAOP=10,000 -YGAPEXT=0,500 -DELOP=6,000
-DELEXT=7,000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
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Search information block:

Query: US-09-294-298-2
Query length: 1423

Database: EST: *

Database sequences: 7991742

Database length: -791223438

Search time (sec): 4.688 750000

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seq_documentation_block:
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DEFINITION Bos taurus brain fetus
Mammalia: Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovidae; Bovinae; Bos.
KEYWORDS cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae.
SOURCE 1 (bases 1 to 571)
AUTHORS Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
Suzuki, H.
TITLE bovine cDNA sequencing
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi Shirakawa, Fukushima 961-8061, Japan
REFERENCE 1
TEL: 81-248-25-5641
FAX: 81-248-25-5725
Email: kazusugi@cooca.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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was deleted from a Not1 site"
124 a 161 c 169 g 116 t 1 others

FEATURES
Source

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musculus C57BL/6J (male) was obtained from the
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnarecs)
was hydrodynamically sheared by repeated passage
0.005 inch orifice at constant velocity. The sheared
DNA was blunt end-repaired with T4 DNA polymerase and
polynucleotide kinase. Adapter oligonucleotides were
ligated to the blunt ends in high molar excess
adapted DNA was purified and size-selected for
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a
of pWd42 (g11473214 (gb AF124072.1)), a copy-number
inducible derivative of plasmid R1. The vector
with adaptors complementary to the insert adaptors
purified. The sheared, adapted mouse DNA was
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene)
and selected for ampicillin resistance."
92 a 151 c 131 g 100 t
BASE COUNT ORIGIN
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255 uAaargpGluLeuProProLysArgTyrTyrCysGluLeuCysLeuA 272
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305 1ArgGalaLeuArgLeuHisLeutyrArgAspSerAspLysLysArgLysL 322
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